

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Om protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 42.1298 Seconds
(without alignments)
(1349.183 Million cell updates/sec)

Title: Perfect score: US-09-939-537-37
Sequence: 591 1 TRFRSRSASPPAYQQGQNQY.....LSTATKDTYDALHQALPPR 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	572	96.8	163	1 CD3Z_PIG
2	561.5	95.0	164	1 CD3Z_HUMAN
3	496	83.9	165	1 CD3Z_RABBIT
4	476.5	80.6	164	1 CD3Z_MOUSE
5	471.5	79.8	166	1 CD3Z_SHEEP
6	378.5	64.0	206	1 CD3Z_MOUSE
7	303	51.3	322	2 06KAV0
8	90.5	15.3	612	2 Q5T8B5
9	90.5	15.3	628	2 Q5TN0B
10	86	14.6	1167	1 WCL_NEUCR
11	86	14.6	1262	2 Q7RTA7
12	85	14.4	172	2 Q8CMD5
13	81.5	13.8	744	2 Q754G7
14	81	13.7	1123	2 Q7KX73
15	80	13.5	692	2 Q19579
16	79.5	13.5	312	2 Q9VYVS
17	78.5	13.3	312	2 Q651R3
18	78	13.3	501	2 Q6U61
19	78	13.2	919	2 Q91DB8
20	78	13.2	937	2 Q9ML4
21	77.5	13.1	328	2 Q6REG4
22	77	13.0	889	2 Q6F4VB
23	77	13.0	928	2 Q6HA9V
24	76.5	12.9	521	1 DB45_DRONC
25	75.5	12.8	169	2 Q8RF77
26	75.5	12.8	169	2 Q8RG33
27	75.5	12.8	169	2 Q8RHV6
28	75.5	12.8	924	2 Q90QJ4
29	75	12.7	171	2 Q8KX22
30	75	12.7	354	2 Q91ES0
31	74.5	12.6	596	2 Q6PA69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ALIGNMENTS

RESULT 1
CD3Z_PIG STANDARD; PRT; 163 AA.
ID CD3Z_PIG
AC QKXSJ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor
DB T3 zeta chain).
GN Name=CD3Z;
OS Sub scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sub.
OC NCBI - TaxID=9823;
RN [1]
RP STRAIN:Minnesota miniature swine;
RC Jie H.-B., Yim D., Kim Y.-B.;
RT "The molecular cloning of porcine CD3 zeta.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Probable role in assembly and expression of the TCR
complex as well as signal transduction upon antigen triggering.
CC -!- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a
TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the
cell surface with the invariant subunits of CD3 labeled gamma,
delta, epsilon, zeta, and eta (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Phosphorylated on Tyr residues after T-cell receptor
triggering (By similarity).
CC -!- SIMILARITY: Belongs to the CD3Z/FCER1G family.
CC -!- SIMILARITY: Contains 3 ITAM domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC DR EMBL; AF15830; AAD4640; -.
DR InterPro; IPR003110; ITAM.
DR Pfam; PF02189; ITAM; 3.
DR SMART; SM00077; ITAM; 3.
FT SIGNAL 1 21
FT CHAIN 22 163
FT DOMAIN 22 30
FT TRANSMEM 31 51
FT DOMAIN 52 163
FT DOMAIN 69 89
FT DOMAIN 107 128
FT DOMAIN 138 158
ITAM 3.

32 74.5 12.6 761 2 QTMNK6
33 74.5 12.6 761 2 Q8DE14
34 74 12.5 136 2 Q39681 daucus caro
35 74 12.5 364 2 Q6C3D3
36 74 12.5 450 2 Q8IE87
37 74 12.5 748 2 Q95TP4 drosophila
38 74 12.5 820 2 Q8CD02
39 74 12.5 867 2 Q8IK17
40 74 12.5 1330 2 Q8K4P0 mus musculus
41 74 12.5 3190 2 Q01368 drosophila
42 74 12.5 3276 2 Q9W321 drosophila
43 73.5 12.4 360 1 Q8PA_BACSU
44 73.5 12.4 360 1 R1PA_YERPE
45 73.5 12.4 360 2 Q66DF1 yersinia pe
Q8zd6 yersinia pe
Q66af1 yersinia pe

FT	DISULFID	32	32	Interchain (Potential). phosphotyrosine (BY Similarity).
FT	MOD-RES	152	152	
SQ	SEQUENCE	163 AA;	18568 MW;	3489620B67167C7 CRC64;
Query Match	Best Local Similarity	96.8%;	Score 572;	DB 1; Length 163;
Matches	107; Conservative	97.3%;	Pred. No. 1.2e-46;	1; Mismatches 2;
OY	2	RFRSRASERPPAYQQCGQNQLNELNIGRREYDVLDRGRDPGKPRKRNPOBGLYNEL	61	
OY	54	KF5RSR5ADAPRQGQCGQNQLNELNIGRREYDVLDRGRDPGKPRKRNPOBGLYNEL	113	
OY	62	QKQKNAEYSEIGNKGERRRKKGHDGLYQGLSTATKDTYDALKHQALPFR	111	
OY	114	QDKMKAEYSEIGNKGERRRKKGHDGLYQGLSTATKDTYDALKHQALPFR	163	
Db				
RESULT 2				
ID	CD3Z_HUMAN	STANDARD;	PRT;	164 AA.
AC	P20963; Q8TQX;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor T3 zeta chain). Name=CD3Z; Synonyms=t3Z, TCRZ;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OC	O'Bryan S.J., Klausner R.D., Weissman A.M., Hou D., Orloff D.G., Modi W.S., Seuanez H., O'Brien S.J., Klausner R.D., Weissman A.M., Hou D., Orloff D.G., Modi W.S., Seuanez H., "Molecular cloning and chromosomal localization of the human T-cell receptor zeta chain: distinction from the molecular CD3 complex."; Proc. Natl. Acad. Sci. U.S.A. 85:9709-9713 (1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8901765; PubMed=2074162;			
RA	Weissman A.M., Hou D., Orloff D.G., Modi W.S., Seuanez H., O'Brien S.J., Klausner R.D., Weissman A.M., Hou D., Orloff D.G., Modi W.S., Seuanez H., "Molecular cloning and chromosomal localization of the human T-cell receptor zeta chain: distinction from the molecular CD3 complex."; Proc. Natl. Acad. Sci. U.S.A. 85:9709-9713 (1988).			
RN				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Berge J.G., Strauberg R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D., Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K., Richards R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Logueillo N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villanueva D.S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blitting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E., Schein J.E., Jones J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;" Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[3]			
RP	INTERACTION WITH HIV-1 NEP.			
RX	PubMed=10242489;			
RA	Xu X.-N., Laffert B., Screeeton G.R., Kraft M., Wolf D., Kolanus W., Mongoliasapay J., McMichael A.J., Baur A.S., "Induction of Fas ligand expression by HIV involves the interaction of Nef with the T cell receptor zeta chain.;" J. Exp. Med. 189:1489-1496 (1999).			
RN	[4]			
RP	INTERACTION WITH SLA.			
RX	MEDLINE=99380595; PubMed=10449770; DOI=10.1073/pnas.96.17.9775;			
RA	Tang J.-H., Sawabikosol S., Chang J.-H., Burkoff S.J.; "STAP, a dimeric adapter protein, plays a functional role in T cell receptor signaling."; Proc. Natl. Acad. Sci. U.S.A. 96:9775-9780 (1999).			
RT	INTERACTION WITH DOCK2.			
RA	MEDLINE=22165501; PubMed=12176041; DOI=10.1016/S0006-291X(02)00931-2;			
RA	Nishihara H., Maeda M., Tsuda M., Makino Y., Sawa H., Nagashima K., Tanaka S.; "DOCK2 mediates T cell receptor-induced activation of Rac2 and IL-2 transcription."; Biochem. Biophys. Res. Commun. 296:716-720 (2002).			
RT	PHOSPHORYLATION SITES TYR-83; TYR-111; TYR-123 AND TYR-142.			
RA	MEDLINE=12522270; DOI=10.1073/pnas.2436191100;			
RA	Salomon A.R., Ficarro S.B., Brill L.M., Brinkley A., Phung Q.T., Ericson C., Sauer K., Brock A., Horn D.M., Schultz P.G., Peters E.C.; "Binding of a high affinity phosphotyrosyl peptide to the Src SH2 domain: crystal structures of the complexed and peptide-free forms."; Proc. Natl. Acad. Sci. U.S.A. 100:443-448 (2003).			
RL	[17]			
RP	STRUCTURE BY NMR OF 136-149.			
RX	MEDLINE=9320050; DOI=10.1016/0092-8674(93)90405-F;			
RA	Waksman G., Shoelson S.E., Pant N., Cowburn D., Kurian J.; "TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the cell surface with the invariant subunits of CD3 labeled gamma, delta, epsilon, zeta, and eta. CD3-zeta forms either homodimers or heterodimers with CD3-eta. Interacts with SIA and SIA2. Interacts with DOCK2. Interacts with HIV-1 Nef protein."; Cell 72:779-790 (1993).			
RT	-!- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the cell surface with the invariant subunits of CD3 labeled gamma, delta, epsilon, zeta, and eta. CD3-zeta forms either homodimers or heterodimers with CD3-eta. Interacts with SIA and SIA2. Interacts with DOCK2. Interacts with HIV-1 Nef protein.			
CC	-!- FUNCTION: Probable role in assembly and expression of the TCR complex as well as signal transduction upon antigen triggering.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=CD3-zeta;			
CC	IsoID=p20963-1; sequence=displayed;			
CC	Name=CD3-eta;			
CC	IsoID=p20963-2; sequence=Not described;			
CC	-!- PTM: Phosphorylated on Tyr residues after T-cell receptor triggering (By similarity).			
CC	-!- SIMILARITY: Belongs to the CD3Z/FCER1G family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).			
CC	EMBL; J04132; AAC60394.1; -.			
DR	EMBL; BC025703; AAH25703.1; -.			
DR	PIR; A31768; A31768.			
DR	DBP; ITGB; NWR; B=136-149.			
DR	GeneDB; HGNC; C=1677; CD3Z.			
DR	H-InvDB; HX0001296; -.			
DR	MIM; 186780; -.			
DR	GO; GO:000586; C:plasma membrane; TAS.			
DR	GO; GO:0042101; C:T-cell receptor complex; TAS.			
DR	GO; GO:005515; Protein binding; IPI.			
DR	GO; GO:0024203; F:protein homodimerization activity; NAS.			
DR	InterPro; IPR003110; ITAM.			
DR	PFAM; PF02189; ITAM; 3.			
DR	SMART; SM00077; ITAM; 3.			
KW	3D-structure; Alternative splicing; Phosphorylation; Receptor; Repeat; Signal; T-cell; transmembrane.			
FT	Signal; 1.			

DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 22-OCT-2004 (Rel. 45, Last annotation update)
 DB T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor
 DB T3 zeta chain).
 GN Name=CD3Z;
 OS Ovis aries (Sheep).
 OC Bovidae; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Buteraria; Detartoiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=White alpine;
 RC MEDLINE=93131305; PubMed=8420837;
 RA Hein W.R., Tunnicliffe A.;
 RT "Invariant components of the sheep T-cell antigen receptor: cloning of the CD3 epsilon and Tcr zeta chains";
 RL Immunogenetics 37:275-284(1993).
 CC -!- FUNCTION: Probable role in assembly and expression of the TCR complex as well as signal transduction upon antigen triggering.
 CC -!- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the cell surface with the invariant subunits of CD3 labeled gamma, delta, epsilon, zeta, and eta.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: Phosphorylated on Tyr residues after T-cell receptor triggering (By similarity).
 CC -!- SIMILARITY: Belongs to the CD3Z/FCER1G family.
 CC -!- SIMILARITY: Contains 3 ITAM domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL: Z12988; CAJ7812.1; -.
 DR PIR: I46424; I46424; ITAM. 3.
 DR InterPro: IPR003110; ITAM.
 DR Pfam: PF0189; ITAM; 3.
 DR SMART: SM00077; ITAM; 3.
 DR Transmembrane.
 FT SIGNAL 1 21 By similarity.
 FT CHAIN 22 166 T-cell surface glycoprotein CD3 zeta chain.
 FT DOMAIN 22 30 Extracellular (Potential).
 FT DOMAIN 31 51 Potential.
 FT DOMAIN 52 166 Cyttoplasmic (Potential).
 FT DOMAIN 69 89 ITAM 1.
 FT DOMAIN 108 129 ITAM 2.
 FT DOMAIN 141 161 ITAM 3.
 FT DISULFID 32 32 Interchain (Potential).
 FT MOD_RES 155 155 Phosphotyrosine (By similarity).
 FT SEQUENCE 166 AA; 18704 MW; E7D89AD84B58311A CRG64;

Query Match 79.8%; Score 471.5; DB 1; Length 166;
 Best Local Similarity 80.5%; Pred. No. 47e-37;
 Matches 91; Conservative 10; Mismatches 9; Indels 3; Gaps 2;

QY 2 RRSRSASPPAYOGONQOLYNELNLGRREBYDVLDKRGKDRPENGKPRRKPNQEGLYNE 60
 Db 54 KRSRSADAPAYQHGQNQVNEINVGRREBYAVALDRRGCFDPWMGGKFQRKQPHVVNE 113
 QY 61 IOKDKMAYAYSIGMK--GERRKGKGKDGlycoglSTATKDTDALMQLPFR 111
 Db 114 LKDKMAYAYSIGMKSDNQRKGKHDGvYQGLSTATKDTDALMQLPFR 166

DR SMART; SM00077; ITAM; 2.
 DR CD3H_MOUSE STANDARD; PRT; 206 AA.
 DR P29020;
 DR 01-DEC-1992 (Rel. 24, Created)
 DR 01-DEC-1992 (Rel. 24, Last sequence update)
 DR 25-OCT-2004 (Rel. 45, Last annotation update)
 DB T-cell surface glycoprotein CD3 eta chain precursor (T-cell receptor
 DB T3 eta chain).
 GN Name=CD3z; Synonym=CD3h;
 GS Mus musculus (Mouse).
 OC Mammalia; Metacoz; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE=90239005; PubMed=2139725;
 RA Jin Y.J., Clayton L.K., Howard F.D., Koyasu S., Sieh M.,
 RA Steinbrich R., Tarr G.B., Reinherz E.L.;
 RT "Molecular cloning of the CD3 eta subunit identifies a CD3 zeta-related product in thymus-derived cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3319-3323 (1990).
 RN [2]
 RP SEQUENCE OF 144-206 FROM N.A.
 RP MEDLINE=91271358; PubMed=1828894;
 RA Clayton L.K., D'Adamo L., Sieh M., Hussey R.B., Koyasu S.,
 RA Reinherz E.L., Howard F.B.,
 RT "CD3 eta and CD3 zeta are alternatively spliced products of a common genetic locus and are transcriptionally and/or post-transcriptionally regulated during T-cell development";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:5202-5206 (1991).
 RL [3]
 RP SEQUENCE OF 144-206 FROM N.A.
 RP MEDLINE=2150596;
 RA Ohno H., Saito T.;
 CC Int. Immunol. 4:1339-1339 (1992).
 CC -!- FUNCTION: Probable role in assembly and expression of the TCR complex as well as signal transduction upon antigen triggering.
 CC -!- SUBUNIT: The TCR/CD3 complex of T lymphocytes consists of either a TCR alpha/beta or TCR gamma/delta heterodimer coexpressed at the cell surface with the invariant subunits of CD3 labeled gamma, delta, epsilon, zeta, and eta. CD3-eta can be complexed in a heterodimeric form with CD3-zeta subunit. CD3-eta homodimer has not been observed.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoform=2;
 CC Name=CD3-zeta;
 CC IsoId=P29020-1; Sequence=Displayed;
 CC Name=CD3-zeta;
 CC IsoId=P24161-1; Sequence=External;
 CC -!- SIMILARITY: Belongs to the CD3Z/FCER1G family.
 CC -!- SIMILARITY: Contains 3 ITAM domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL: M33158; AAA73098.1; -.
 DR M76711; AA40403.1; -.
 DR PIR: A35900; A35900.
 DR MGD: MGI:88334; Cd3z.
 DR InterPro: IPR003110; ITAM.
 DR Pfam: PF02189; ITAM; 2.

RESULT 6
 CD3H_MOUSE

KW Alternative splicing; Direct protein sequencing; Receptor; Repeat;
 KW Signal; T-cell; Transmembrane.
 FT SIGNAL; 1; 21
 FT CHAIN; 22; 206 T-cell surface glycoprotein CD3 eta
 FT DOMAIN; 22; 30 Extracellular chain.
 FT TRANSMEM 31; 51 Extracellular (potential).
 FT DOMAIN; 52; 206 Potential (potential).
 FT DOMAIN; 69; 129 Cytoplasmic (potential).
 PT DOMAIN; 108; 129 ITAM 1.
 PT DOMAIN; 139; 159 ITAM 2.
 PT DISULFID 32; 32 ITAM 3.
 SQ SEQUENCE 206 AA; 23339 MW; 829256A2C94E444 CRC64;
 Query Match 64.0%; Score 378.5; DB 1; Length 206;
 Best Local Similarity 82.2%; Pred. No. 43e-28;
 Matches 74; Conservative 5; Mismatches 10; Indels 1; Gaps 1;
 QY 2 RRSRSAPPAYQOGQONLYNENLGRREYVLDKRGGRDPGMGK-PRRKPOEGLYNE 60
 DB 54 KRSRSADAPAYQOGQONLYNENLGRREYVLDKRGGRDPGMGK-PRRKPOEGLYNE 113
 QY 61 LQDKMAYEAYSETGMKBERRRKGHDGLYQ 90
 DB 114 LQDKMAYEAYSETGMKBERRRKGHDGLYQ 143
 RESULT 7
 ID 06KAV0 PRELIMINARY; PRT; 322 AA.
 AC 06KAV0;
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DE Hypothetical protein FLJ46519.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RA Niromiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kambara K.,
 RA Katsura N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 RA Yamashita H., Matsuo K., Nakamura Y., Sekine H., Kikuchi H.,
 RA Murakawa K., Kamehori K., Takahashi-Fujii A., Oshina A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RIL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK129376; BAC894707; 1.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005888; P:transmembrane receptor activity; IEA.
 DR GO; GO:007166; P:cell surface receptor linked signal transdu. . .; IEA.
 DR InterPro; IPR003110; ITAM.
 DR Pfam; PF02189; ITAM; 1.
 DR SMART; SM0077; ITAM; 1.
 DR SMART; SM00233; PH; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR SEQUENCE 322 AA; 34926 MW; D4461DBEC26BC011 CRC64;
 SQ Query Match 51.3%; Score 303; DB 2; Length 322;
 Best Local Similarity 60.5%; Pred. No. 1.1e-20;
 Matches 69; Conservative 9; Mismatches 12; Indels 24; Gaps 6;
 QY 2 RRSRSAPPAYQOGQONLYNENLGRREYVLDKRGGRDPGMGK-PRRKPOEGLYNE 60
 DB 54 KRSRSADAPAYQOGQONLYNENLGRREYVLDKRGGRDPGMGK-PRRKPOEGLYNE 113
 QY 61 LQDKMAYEAYSETGMKBERRRKGHDGLYQ 90
 DB 114 SREDLTFDGLKGKLEGLER-GSRRGAGGRGGGLQRKGPRKGKRAPERGEGL 166
 RESULT 8
 Q7SYBS PRELIMINARY; PRT; 612 AA.
 ID Q7SYBS
 AC Q7SYBS
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DE Similar to differentially expressed in FDCP 6.
 GN ORFName=ZGC:63711;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Actinopterygi; Neopterygi; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID:7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12479732; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schnuler G.D.,
 RA Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordon H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prang C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarino P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green D.E., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PHE domain.
 DR EMBL; BC054935; AAH54935; 1; -.
 DR HSSP; O08967; 1FGY.
 DR ZFIN; ZDB-GENE-040426-1246; zgc:63721.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; BP_Hand_like.
 DR InterPro; IPR011849; PH.
 DR InterPro; IPR011036; PH_related.
 DR Pfam; PF00169; PH; 1.
 DR SMART; SM00233; PH; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR SEQUENCE 612 AA; 72090 MW; 778DBDC5FBEBB689 CRC64;
 SQ Query Match 15.3%; Score 90.5; DB 2; Length 612;
 Best Local Similarity 28.3%; Pred. No. 4.2; Mismatches 43; Indels 3; Gaps 3;
 Matches 28; Conservative 25; Mismatches 43; Indels 3; Gaps 3;
 QY 12 YQQGQONLYNENLGRREYVLDKRGGRDPGMGK-PRRKPOEGLYNE 70
 DB 309 YVEGKTSLHKDQLKRGGRDPGMGK-PRRKPOEGLYNE 368
 QY 71 SBRGM-KGERKGKGDGLYQGLSTATKTDYD-LIMQ 107
 DB 369 QAMLBODBQRROQHQHOLHOALEIOLKEABRASMQA 407
 RESULT 9
 Q6TNUB

GN Name=NCTU02356_1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariidae; Sordariales; Sordariaceae; Neurospora.
 OC NCBI_TAXID=5141;
 RN [1]
 SEQUENCE FROM N.A.
 RP
 RC STRAIN=OR74A;
 RA Galagan J.B., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 Jaffé D., FitzHugh W., Ma L.-J., Smilovic S., Purcell S., Rehman B.,
 Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 Qui B., Tarkkiev P., Pedersen D., Nelson M., Washburne M.,
 Selitrennikoff C.P., Kinney J.A., Braun E.L., Zeltner A., Schulte U.,
 Kotche G.O., Jedd G., Mees W., Staben C., Marcotte B., Greenberg D.,
 Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gherre S.,
 Kamal M., Kamysyssels M., Mauceli E., Rudd S., Krishnan D.,
 Krylosova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
 Ra Cogoni C., Macino G., Cattoni D., Li W., Pratt R.J., Osman S.A.,
 Ra Desouza C.C., Glass J., Orbach M.J., Berglund J.J., Voelker R.,
 Ra Yarden O., Plamann M., Seiller S., Dunlap J., Radford A., Aramayo R.,
 Ra Paulsen I., Sachis M., Hander E.S., Nusbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*."
 RL Nature 0:00 (2003).
 CC -|- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR BSSP; P17679; 1CNP.
 DR ABX0100358; RA30541.1; -.
 DR InterPro; IPR000345; Cytc_heme_BS.
 DR GO; GO:00534; C:nuclieus; IEA.
 DR GO; GO:000481; F:transcription factor activity; IEA.
 DR GO; GO:000335; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:000165; P:signal transduction; IEA.
 DR InterPro; IPR000160; PAC.
 DR InterPro; IPR000014; PAS.
 DR PF00120; GATA; 1.
 DR Pfam; PF00185; PAC; 1.
 DR TIGR00229; sensory box; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00344; GATA_ZN_FINGER_1; 1.
 DR PROSITE; PS00114; GATA_ZN_FINGER_2; 1.
 DR PROSITE; PS00112; PAS_3; 1.
 DR SEQUENCE 1262 AA; 138115 MW; F39E72B09DE1E5F1 CRC64;
 Query Match 14.6%; Score 85; DB 2; Length 1262;
 Best Local Similarity 24.8%; Pred. No. 1; Mismatches 19; Indels 49; Gaps 6;
 Matches 33; Conservative 19; Mismatches 49; Indels 32; Gaps 6;
 QY 9 PAVQVQGQNOLY-----NENLNGRREIVDVLDRKRGDPWMGSKPQR-----KN 52
 Db 71 PPTINQGNSTIHASDVTMGGGSISLDLTIQQNIDEMHRRSPVHPOPGQQTTRLSMEDYAN 130
 QY 53 PQEGLYNELQDKDQKAYSE---IGMKGERRKGK-----HDGJXQGS---TATK 97
 Db 131 PNDG-FSDYQLDNNMSGNYQDMGGMGSQHSFQAGQNMAMDHSGGYSHSPNVMGNM 189
 QY 98 DTYDALHMQALPP 110
 Db 190 MTPNPNMTHSPP 202
 RESULT 12
 Q8CMD5 PRELIMINARY; PRT; 172 AA.
 ID Q8CMD5
 AC Q8CMD5;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DT Hypothetical protein SMU.566c (Hypothetical protein SMU.1379)
 DB (Hypothetical protein SMU.1408c) (Hypothetical protein
 SMU.1894c);
 DE SMU.1894c).
 OC Order-locusnames=SMU.1379, SMU.1408c, SMU.566c, SMU.766;
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus;
 OC NCBI_TAXID=1309;
 RN [1]
 SEQUENCE FROM N.A.
 RP
 RC STRAIN=U159 / ATCC 700610 / Serotype C;
 RX MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
 RA Carson M.B., Primeaux C., Tran R., Kenton S., Jia H.G., Lin S.P.,
 Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 Qian Y., Li S., Zhu H., Najar F.Z., Iai H., White J., Roe B.A.,
 RA Ferretti J.J.;
 RT "Genome sequence of *Streptococcus mutans* U159, a cariogenic dental
 pathogen,"
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
 DR EMBL; AE014901; AAMS8307.1; -.
 DR EMBL; AE014918; AAMS8486.1; -.
 DR EMBL; AE014971; AAMS9047.1; -.
 DR EMBL; AE014974; AAMS9073.1; -.
 DR EMBL; AE015015; AAMS9507.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004803; F:transposase activity; IEA.
 DR GO; GO:0006313; P:DNA transposition; IEA.
 DR InterPro; IPR00957; Homeodomain_1ike.
 DR InterPro; IPR002514; Transposase_8.
 DR Pfam; PF01527; Transposase_8; 1.
 DR KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 172 AA; 20622 MW; 5187DC04B6407F52 CRC64;
 Query Match 14.4%; Score 85; DB 2; Length 172;
 Best Local Similarity 36.8%; Pred. No. 3.1; Mismatches 14; Conservative 12; Mismatches 12; Indels 0; Gaps 0; Matches 14; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
 QY 27 RREYYDVLDRKRGDPWMGSKPQRKNPQEGLYNEQD 64
 Db 100 KKNRYTIVEKTRGRPPKMKRKPKKSEEMTLEQIQLKE 137
 RESULT 13
 Q754G7 PRELIMINARY; PRT; 744 AA.
 ID Q754G7
 AC Q754G7
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE AFR10WP.
 GN Name=AFR103W;
 OS Ashbya gossypii (Yeast) (Bremothecium gossypii);
 OC Bacteria; Fungi; Ascomycota; Saccharomycetaceae; Bremothecium.
 OC NCBI_TAXID=33169;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 RA Garfney T.D., Philippson P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome.";
 RL Science 304:304-307 (2004).
 DR EMBL; AE016901; AAS53474.1; -.
 DR AGD; AFR103W; -
 DR InterPro; IPR010983; BP_Hand_like.
 DR InterPro; IPR000261; BPS15_homology.
 DR SMART; SM0027; EH; 1.
 DR PROSITE; PS00031; EH; 1.
 SQ SEQUENCE 744 AA; 82630 MW; 7D8E05484729D7D1 CRC64;
 Query Match 13.8%; Score 81.5; DB 2; Length 744;

This Page Blank (uspto)